

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: BASF Aktiengesellschaft
 - (B) STREET:
 - (C) CITY: Ludwigshafen
 - (E) COUNTRY: Deutschland
 - (F) POSTAL CODE (ZIP): 67065
- (ii) TITLE OF INVENTION: Neue Poly ADP Ribose Polymerase Gene
- (iii) NUMBER OF SEQUENCES: 28
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC DOS/MS DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1843 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 3..1715
 - (D) OTHER INFORMATION: /product= "Poly ADP Ribose Polymerase"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CC ATG GCG GCG CGG CGG CGA CGG AGC ACC GGC GGC GGC AGG GCG AGA	47
Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg	
1 5 10 15	
GCA TTA AAT GAA AGC AAA AGA GTT AAT AAT GGC AAC ACG GCT CCA GAA	95
Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu	
20 25 30	

GAC TCT TCC CCT GCC AAG AAA ACT CGT AGA TGC CAG AGA CAG GAG TCG	143
Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser	
35 40 45	
AAA AAG ATG CCT GTG GCT GGA GGA AAA GCT AAT AAG GAC AGG ACA GAA	191
Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu	
50 55 60	
GAC AAG CAA GAT GAA TCT GTG AAG GCC TTG CTG TTA AAG GGC AAA GCT	239
Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala	
65 70 75	
CCT GTG GAC CCA GAG TGT ACA GCC AAG GTG GGG AAG GCT CAT GTG TAT	287
Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr	
80 85 90 95	
TGT GAA GGA AAT GAT GTC TAT GAT GTC ATG CTA AAT CAG ACC AAT CTC	335
Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu	
100 105 110	
CAG TTC AAC AAC AAC AAG TAC TAT CTG ATT CAG CTA TTA GAA GAT GAT	383
Gln Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp	
115 120 125	
GCC CAG AGG AAC TTC AGT GTT TGG ATG AGA TGG GGC CGA GTT GGG AAA	431
Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys	
130 135 140	
ATG GGA CAG CAC AGC CTG GTG GCT TGT TCA GGC AAT CTC AAC AAG GCC	479
Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala	
145 150 155	
AAG GAA ATC TTT CAG AAG AAA TTC CTT GAC AAA ACG AAA AAC AAT TGG	527
Lys Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp	
160 165 170 175	
GAA GAT CGA GAA AAG TTT GAG AAG GTG CCT GGA AAA TAT GAT ATG CTA	575
Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu	
180 185 190	
CAG ATG GAC TAT GCC ACC AAT ACT CAG GAT GAA GAG GAA ACA AAG AAA	623
Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys	
195 200 205	
GAG GAA TCT CTT AAA TCT CCC TTG AAG CCA GAG TCA CAG CTA GAT CTT	671
Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu	
210 215 220	
CGG GTA CAG GAG TTA ATA AAG TTG ATC TGT AAT GTT CAG GCC ATG GAA	719
Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu	
225 230 235	
GAA ATG ATG ATG GAA ATG AAG TAT AAT ACC AAG AAA GCC CCA CTT GGG	767
Glu Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly	
240 245 250 255	
AAG CTG ACA GTG GCA CAA ATC AAG GCA GGT TAC CAG TCT CTT AAG AAG	815
Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys	

260										265										270										
ATT	GAG	GAT	TGT	ATT	CGG	GCT	GGC	CAG	CAT	GGA	CGA	GCT	CTC	ATG	GAA															863
Ile	Glu	Asp	Cys	Ile	Arg	Ala	Gly	Gln	His	Gly	Arg	Ala	Leu	Met	Glu															
			275					280					285																	
GCA	TGC	AAT	GAA	TTC	TAC	ACC	AGG	ATT	CCG	CAT	GAC	TTT	GGA	CTC	CGT															911
Ala	Cys	Asn	Glu	Phe	Tyr	Thr	Arg	Ile	Pro	His	Asp	Phe	Gly	Leu	Arg															
			290				295					300																		
ACT	CCT	CCA	CTA	ATC	CGG	ACA	CAG	AAG	GAA	CTG	TCA	GAA	AAA	ATA	CAA															959
Thr	Pro	Pro	Leu	Ile	Arg	Thr	Gln	Lys	Glu	Leu	Ser	Glu	Lys	Ile	Gln															
			305				310				315																			
TTA	CTA	GAG	GCT	TTG	GGA	GAC	ATT	GAA	ATT	GCT	ATT	AAG	CTG	GTG	AAA															1007
Leu	Leu	Glu	Ala	Leu	Gly	Asp	Ile	Glu	Ile	Ala	Ile	Lys	Leu	Val	Lys															
			320			325				330					335															
ACA	GAG	CTA	CAA	AGC	CCA	GAA	CAC	CCA	TTG	GAC	CAA	CAC	TAT	AGA	AAC															1055
Thr	Glu	Leu	Gln	Ser	Pro	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg	Asn															
				340				345						350																
CTA	CAT	TGT	GCC	TTG	CGC	CCC	CTT	GAC	CAT	GAA	AGT	TAC	GAG	TTC	AAA															1103
Leu	His	Cys	Ala	Leu	Arg	Pro	Leu	Asp	His	Glu	Ser	Tyr	Glu	Phe	Lys															
			355					360					365																	
GTG	ATT	TCC	CAG	TAC	CTA	CAA	TCT	ACC	CAT	GCT	CCC	ACA	CAC	AGC	GAC															1151
Val	Ile	Ser	Gln	Tyr	Leu	Gln	Ser	Thr	His	Ala	Pro	Thr	His	Ser	Asp															
			370				375					380																		
TAT	ACC	ATG	ACC	TTG	CTG	GAT	TTG	TTT	GAA	GTG	GAG	AAG	GAT	GGT	GAG															1199
Tyr	Thr	Met	Thr	Leu	Leu	Asp	Leu	Phe	Glu	Val	Glu	Lys	Asp	Gly	Glu															
			385			390					395																			
AAA	GAA	GCC	TTC	AGA	GAG	GAC	CTT	CAT	AAC	AGG	ATG	CTT	CTA	TGG	CAT															1247
Lys	Glu	Ala	Phe	Arg	Glu	Asp	Leu	His	Asn	Arg	Met	Leu	Leu	Trp	His															
					405				410						415															
GGT	TCC	AGG	ATG	AGT	AAC	TGG	GTG	GGA	ATC	TTG	AGC	CAT	GGG	CTT	CGA															1295
Gly	Ser	Arg	Met	Ser	Asn	Trp	Val	Gly	Ile	Leu	Ser	His	Gly	Leu	Arg															
				420				425					430																	
ATT	GCC	CCA	CCT	GAA	GCT	CCC	ATC	ACA	GGT	TAC	ATG	TTT	GGG	AAA	GGA															1343
Ile	Ala	Pro	Pro	Glu	Ala	Pro	Ile	Thr	Gly	Tyr	Met	Phe	Gly	Lys	Gly															
			435				440					445																		
ATC	TAC	TTT	GCT	GAC	ATG	TCT	TCC	AAG	AGT	GCC	AAT	TAC	TGC	TTT	GCC															1391
Ile	Tyr	Phe	Ala	Asp	Met	Ser	Ser	Lys	Ser	Ala	Asn	Tyr	Cys	Phe	Ala															
			450				455					460																		
TCT	CGC	CTA	AAG	AAT	ACA	GGA	CTG	CTG	CTC	TTA	TCA	GAG	GTA	GCT	CTA															1439
Ser	Arg	Leu	Lys	Asn	Thr	Gly	Leu	Leu	Leu	Leu	Ser	Glu	Val	Ala	Leu															
			465			470					475																			
GGT	CAG	TGT	AAT	GAA	CTA	CTA	GAG	GCC	AAT	CCT	AAG	GCC	GAA	GGA	TTG															1487
Gly	Gln	Cys	Asn	Glu	Leu	Leu	Glu	Ala	Asn	Pro	Lys	Ala	Glu	Gly	Leu															
					485				490						495															
CTT	CAA	GGT	AAA	CAT	AGC	ACC	AAG	GGG	CTG	GGC	AAG	ATG	GCT	CCC	AGT															1535

Leu	Gln	Gly	Lys	His	Ser	Thr	Lys	Gly	Leu	Gly	Lys	Met	Ala	Pro	Ser			
				500					505					510				
TCT	GCC	CAC	TTC	GTC	ACC	CTG	AAT	GGG	AGT	ACA	GTG	CCA	TTA	GGA	CCA		1583	
Ser	Ala	His	Phe	Val	Thr	Leu	Asn	Gly	Ser	Thr	Val	Pro	Leu	Gly	Pro			
			515					520					525					
GCA	AGT	GAC	ACA	GGA	ATT	CTG	AAT	CCA	GAT	GGT	TAT	ACC	CTC	AAC	TAC		1631	
Ala	Ser	Asp	Thr	Gly	Ile	Leu	Asn	Pro	Asp	Gly	Tyr	Thr	Leu	Asn	Tyr			
		530					535					540						
AAT	GAA	TAT	ATT	GTA	TAT	AAC	CCC	AAC	CAG	GTC	CGT	ATG	CGG	TAC	CTT		1679	
Asn	Glu	Tyr	Ile	Val	Tyr	Asn	Pro	Asn	Gln	Val	Arg	Met	Arg	Tyr	Leu			
	545						550				555							
TTA	AAG	GTT	CAG	TTT	AAT	TTC	CTT	CAG	CTG	TGG	TGA	ATGTTGATAT					1725	
Leu	Lys	Val	Gln	Phe	Asn	Phe	Leu	Gln	Leu	Trp	*							
	560					565				570								
TAAATAAACC	AGAGATCTGA	TCTTCAAGCA	AGAAAATAAG	CAGTGTGTGTA	CTTGTGAATT												1785	
TTGTGATATT	TTATGTAATA	AAACTGTAC	AGGTCTAAAA	AAAAAAAAAA	AAAAAAAAAA												1843	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Ala	Arg	Arg	Arg	Arg	Ser	Thr	Gly	Gly	Gly	Arg	Ala	Arg	Ala		
1				5					10					15			
Leu	Asn	Glu	Ser	Lys	Arg	Val	Asn	Asn	Gly	Asn	Thr	Ala	Pro	Glu	Asp		
			20					25					30				
Ser	Ser	Pro	Ala	Lys	Lys	Thr	Arg	Arg	Cys	Gln	Arg	Gln	Glu	Ser	Lys		
		35				40						45					
Lys	Met	Pro	Val	Ala	Gly	Gly	Lys	Ala	Asn	Lys	Asp	Arg	Thr	Glu	Asp		
	50				55						60						
Lys	Gln	Asp	Glu	Ser	Val	Lys	Ala	Leu	Leu	Leu	Lys	Gly	Lys	Ala	Pro		
	65				70				75						80		
Val	Asp	Pro	Glu	Cys	Thr	Ala	Lys	Val	Gly	Lys	Ala	His	Val	Tyr	Cys		
			85						90					95			
Glu	Gly	Asn	Asp	Val	Tyr	Asp	Val	Met	Leu	Asn	Gln	Thr	Asn	Leu	Gln		
		100						105					110				
Phe	Asn	Asn	Asn	Lys	Tyr	Tyr	Leu	Ile	Gln	Leu	Leu	Glu	Asp	Asp	Ala		
	115						120					125					
Gln	Arg	Asn	Phe	Ser	Val	Trp	Met	Arg	Trp	Gly	Arg	Val	Gly	Lys	Met		

130					135					140					
Gly	Gln	His	Ser	Leu	Val	Ala	Cys	Ser	Gly	Asn	Leu	Asn	Lys	Ala	Lys
145					150					155					160
Glu	Ile	Phe	Gln	Lys	Lys	Phe	Leu	Asp	Lys	Thr	Lys	Asn	Asn	Trp	Glu
				165					170					175	
Asp	Arg	Glu	Lys	Phe	Glu	Lys	Val	Pro	Gly	Lys	Tyr	Asp	Met	Leu	Gln
			180					185					190		
Met	Asp	Tyr	Ala	Thr	Asn	Thr	Gln	Asp	Glu	Glu	Glu	Thr	Lys	Lys	Glu
			195				200					205			
Glu	Ser	Leu	Lys	Ser	Pro	Leu	Lys	Pro	Glu	Ser	Gln	Leu	Asp	Leu	Arg
	210					215					220				
Val	Gln	Glu	Leu	Ile	Lys	Leu	Ile	Cys	Asn	Val	Gln	Ala	Met	Glu	Glu
225					230					235					240
Met	Met	Met	Glu	Met	Lys	Tyr	Asn	Thr	Lys	Lys	Ala	Pro	Leu	Gly	Lys
				245					250					255	
Leu	Thr	Val	Ala	Gln	Ile	Lys	Ala	Gly	Tyr	Gln	Ser	Leu	Lys	Lys	Ile
			260					265					270		
Glu	Asp	Cys	Ile	Arg	Ala	Gly	Gln	His	Gly	Arg	Ala	Leu	Met	Glu	Ala
		275					280					285			
Cys	Asn	Glu	Phe	Tyr	Thr	Arg	Ile	Pro	His	Asp	Phe	Gly	Leu	Arg	Thr
	290					295					300				
Pro	Pro	Leu	Ile	Arg	Thr	Gln	Lys	Glu	Leu	Ser	Glu	Lys	Ile	Gln	Leu
305					310					315					320
Leu	Glu	Ala	Leu	Gly	Asp	Ile	Glu	Ile	Ala	Ile	Lys	Leu	Val	Lys	Thr
				325					330					335	
Glu	Leu	Gln	Ser	Pro	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg	Asn	Leu
			340					345					350		
His	Cys	Ala	Leu	Arg	Pro	Leu	Asp	His	Glu	Ser	Tyr	Glu	Phe	Lys	Val
		355					360					365			
Ile	Ser	Gln	Tyr	Leu	Gln	Ser	Thr	His	Ala	Pro	Thr	His	Ser	Asp	Tyr
	370					375					380				
Thr	Met	Thr	Leu	Leu	Asp	Leu	Phe	Glu	Val	Glu	Lys	Asp	Gly	Glu	Lys
385					390					395					400
Glu	Ala	Phe	Arg	Glu	Asp	Leu	His	Asn	Arg	Met	Leu	Leu	Trp	His	Gly
				405				410						415	
Ser	Arg	Met	Ser	Asn	Trp	Val	Gly	Ile	Leu	Ser	His	Gly	Leu	Arg	Ile
			420					425					430		
Ala	Pro	Pro	Glu	Ala	Pro	Ile	Thr	Gly	Tyr	Met	Phe	Gly	Lys	Gly	Ile
			435				440					445			
Tyr	Phe	Ala	Asp	Met	Ser	Ser	Lys	Ser	Ala	Asn	Tyr	Cys	Phe	Ala	Ser

450	455	460
Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu Gly		
465	470	475 480
Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu		
	485 490	495
Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser		
	500 505	510
Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala		
	515 520	525
Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn		
	530 535	540
Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu		
	545 550	555 560
Lys Val Gln Phe Asn Phe Leu Gln Leu Trp *		
	565 570	

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:

- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 242..1843
- (D) OTHER INFORMATION: /product= "Poly ADP Ribose Polymerase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGGGACTGGT CGCCTGACTC GGCCTGCCCC AGCCTCTGCT TCACCCCACT GGTGGCCAAA	60
TAGCCGATGT CTAATCCCC ACACAAGCTC ATCCCCGGCC TCTGGGATTG TTGGGAATTC	120
TCTCCCTAAT TCACGCCTGA GGCTCATGGA GAGTTGCTAG ACCTGGGACT GCCCTGGGAG	180
GCGCACACAA CCAGGCCGGG TGGCAGCCAG GACCTCTCCC ATGTCCCTGC TTTTCTTGGC	240
C ATG GCT CCA AAG CCG AAG CCC TGG GTA CAG ACT GAG GGC CCT GAG	286
Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu	

575										580					585					
AAG	AAG	AAG	GGC	CGG	CAG	GCA	GGA	AGG	GAG	GAG	GAC	CCC	TTC	CGC	TCC		334			
Lys	Lys	Lys	Gly	Arg	Gln	Ala	Gly	Arg	Glu	Glu	Asp	Pro	Phe	Arg	Ser					
			590					595					600							
ACC	GCT	GAG	GCC	CTC	AAG	GCC	ATA	CCC	GCA	GAG	AAG	CGC	ATA	ATC	CGC		382			
Thr	Ala	Glu	Ala	Leu	Lys	Ala	Ile	Pro	Ala	Glu	Lys	Arg	Ile	Ile	Arg					
		605					610					615								
GTG	GAT	CCA	ACA	TGT	CCA	CTC	AGC	AGC	AAC	CCC	GGG	ACC	CAG	GTG	TAT		430			
Val	Asp	Pro	Thr	Cys	Pro	Leu	Ser	Ser	Asn	Pro	Gly	Thr	Gln	Val	Tyr					
	620					625					630									
GAG	GAC	TAC	AAC	TGC	ACC	CTG	AAC	CAG	ACC	AAC	ATC	GAG	AAC	AAC	AAC		478			
Glu	Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Glu	Asn	Asn	Asn					
635					640					645					650					
AAC	AAG	TTC	TAC	ATC	ATC	CAG	CTG	CTC	CAA	GAC	AGC	AAC	CGC	TTC	TTC		526			
Asn	Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln	Asp	Ser	Asn	Arg	Phe	Phe					
				655					660					665						
ACC	TGC	TGG	AAC	CGC	TGG	GGC	CGT	GTG	GGA	GAG	GTC	GGC	CAG	TCA	AAG		574			
Thr	Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	Lys					
			670					675					680							
ATC	AAC	CAC	TTC	ACA	AGG	CTA	GAA	GAT	GCA	AAG	AAG	GAC	TTT	GAG	AAG		622			
Ile	Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Glu	Lys					
		685					690					695								
AAA	TTT	CGG	GAA	AAG	ACC	AAG	AAC	AAC	TGG	GCA	GAG	CGG	GAC	CAC	TTT		670			
Lys	Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp	Ala	Glu	Arg	Asp	His	Phe					
	700					705					710									
GTG	TCT	CAC	CCG	GGC	AAG	TAC	ACA	CTT	ATC	GAA	GTA	CAG	GCA	GAG	GAT		718			
Val	Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Ala	Glu	Asp					
	715				720					725					730					
GAG	GCC	CAG	GAA	GCT	GTG	GTG	AAG	GTG	GAC	AGA	GGC	CCA	GTG	AGG	ACT		766			
Glu	Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp	Arg	Gly	Pro	Val	Arg	Thr					
				735					740					745						
GTG	ACT	AAG	CGG	GTG	CAG	CCC	TGC	TCC	CTG	GAC	CCA	GCC	ACG	CAG	AAG		814			
Val	Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Lys					
			750					755						760						
CTC	ATC	ACT	AAC	ATC	TTC	AGC	AAG	GAG	ATG	TTC	AAG	AAC	ACC	ATG	GCC		862			
Leu	Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Thr	Met	Ala					
			765				770					775								
CTC	ATG	GAC	CTG	GAT	GTG	AAG	AAG	ATG	CCC	CTG	GGA	AAG	CTG	AGC	AAG		910			
Leu	Met	Asp	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Ser	Lys					
	780					785					790									
CAA	CAG	ATT	GCA	CGG	GGT	TTC	GAG	GCC	TTG	GAG	GCG	CTG	GAG	GAG	GCC		958			
Gln	Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala					
	795				800					805					810					
CTG	AAA	GGC	CCC	ACG	GAT	GGT	GGC	CAA	AGC	CTG	GAG	GAG	CTG	TCC	TCA		1006			

Leu	Lys	Gly	Pro	Thr	Asp	Gly	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser		
				815					820					825			
CAC	TTT	TAC	ACC	GTC	ATC	CCG	CAC	AAC	TTC	GGC	CAC	AGC	CAG	CCC	CCG	1054	
His	Phe	Tyr	Thr	Val	Ile	Pro	His	Asn	Phe	Gly	His	Ser	Gln	Pro	Pro		
			830					835					840				
CCC	ATC	AAT	TCC	CCT	GAG	CTT	CTG	CAG	GCC	AAG	AAG	GAC	ATG	CTG	CTG	1102	
Pro	Ile	Asn	Ser	Pro	Glu	Leu	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu		
		845					850					855					
GTG	CTG	GCG	GAC	ATC	GAG	CTG	GCC	CAG	GCC	CTG	CAG	GCA	GTC	TCT	GAG	1150	
Val	Leu	Ala	Asp	Ile	Glu	Leu	Ala	Gln	Ala	Leu	Gln	Ala	Val	Ser	Glu		
	860					865					870						
CAG	GAG	AAG	ACG	GTG	GAG	GAG	GTG	CCA	CAC	CCC	CTG	GAC	CGA	GAC	TAC	1198	
Gln	Glu	Lys	Thr	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr		
875				880				885							890		
CAG	CTT	CTC	AAG	TGC	CAG	CTG	CAG	CTG	CTA	GAC	TCT	GGA	GCA	CCT	GAG	1246	
Gln	Leu	Leu	Lys	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly	Ala	Pro	Glu		
				895				900						905			
TAC	AAG	GTG	ATA	CAG	ACC	TAC	TTA	GAA	CAG	ACT	GGC	AGC	AAC	CAC	AGG	1294	
Tyr	Lys	Val	Ile	Gln	Thr	Tyr	Leu	Glu	Gln	Thr	Gly	Ser	Asn	His	Arg		
			910					915					920				
TGC	CCT	ACA	CTT	CAA	CAC	ATC	TGG	AAA	GTA	AAC	CAA	GAA	GGG	GAG	GAA	1342	
Cys	Pro	Thr	Leu	Gln	His	Ile	Trp	Lys	Val	Asn	Gln	Glu	Gly	Glu	Glu		
		925					930					935					
GAC	AGA	TTC	CAG	GCC	CAC	TCC	AAA	CTG	GGT	AAT	CGG	AAG	CTG	CTG	TGG	1390	
Asp	Arg	Phe	Gln	Ala	His	Ser	Lys	Leu	Gly	Asn	Arg	Lys	Leu	Leu	Trp		
	940					945					950						
CAT	GGC	ACC	AAC	ATG	GCC	GTG	GTG	GCC	GCC	ATC	CTC	ACT	AGT	GGG	CTC	1438	
His	Gly	Thr	Asn	Met	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu		
955					960					965					970		
CGC	ATC	ATG	CCA	CAT	TCT	GGT	GGG	CGT	GTT	GGC	AAG	GGC	ATC	TAC	TTT	1486	
Arg	Ile	Met	Pro	His	Ser	Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe		
				975				980						985			
GCC	TCA	GAG	AAC	AGC	AAG	TCA	GCT	GGA	TAT	GTT	ATT	GGC	ATG	AAG	TGT	1534	
Ala	Ser	Glu	Asn	Ser	Lys	Ser	Ala	Gly	Tyr	Val	Ile	Gly	Met	Lys	Cys		
			990					995					1000				
GGG	GCC	CAC	CAT	GTC	GGC	TAC	ATG	TTC	CTG	GGT	GAG	GTG	GCC	CTG	GGC	1582	
Gly	Ala	His	His	Val	Gly	Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly		
		1005					1010					1015					
AGA	GAG	CAC	CAT	ATC	AAC	ACG	GAC	AAC	CCC	AGC	TTG	AAG	AGC	CCA	CCT	1630	
Arg	Glu	His	His	Ile	Asn	Thr	Asp	Asn	Pro	Ser	Leu	Lys	Ser	Pro	Pro		
	1020					1025					1030						
CCT	GGC	TTC	GAC	AGT	GTC	ATT	GCC	CGA	GGC	CAC	ACC	GAG	CCT	GAT	CCG	1678	
Pro	Gly	Phe	Asp	Ser	Val	Ile	Ala	Arg	Gly	His	Thr	Glu	Pro	Asp	Pro		
1035					1040					1045					1050		

ACC CAG GAC ACT GAG TTG GAG CTG GAT GGC CAG CAA GTG GTG GTG CCC	1726
Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro	
1055 1060 1065	
CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC TCC	1774
Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser	
1070 1075 1080	
CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC TAC	1822
Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr	
1085 1090 1095	
CTG CTG GAG GTC CAC CTC TGA GTGCCCCGCC TGTCCCCCGG GGTCTGCAA	1873
Leu Leu Glu Val His Leu *	
1100 1105	
GGCTGGACTG TGATCTTCAA TCATCCTGCC CATCTCTGGT ACCCCTATAT CACTCCTTTT	1933
TTTCAAGAAT ACAATACGTT GTTGTTAACT ATAGTCACCA TGCTGTACAA GATCCCTGAA	1993
CTTATGCCTC CTAAGTAAAA TTTTGTATTC TTTGACACAT CTGCCCAGTC CCTCTCCTCC	2053
CAGCCCATGG TAACCAGCAT TTGACTCTTT ACTTGTATAA GGGCAGCTTT TATAGGTTCC	2113
ACATGTAAGT GAGATCATGC AGTGTTTGTC TTTCTGTGCC TGGCTTATTT CACTCAGCAT	2173
AATGTGCACC GGGTTCACCC ATGTTTTTCAT AAATGACAAG ATTTCTCCT TAAAAA	2233
AAAAA	2265

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Ala	Pro	Lys	Pro	Lys	Pro	Trp	Val	Gln	Thr	Glu	Gly	Pro	Glu	Lys
1				5					10					15	
Lys	Lys	Gly	Arg	Gln	Ala	Gly	Arg	Glu	Glu	Asp	Pro	Phe	Arg	Ser	Thr
		20						25					30		
Ala	Glu	Ala	Leu	Lys	Ala	Ile	Pro	Ala	Glu	Lys	Arg	Ile	Ile	Arg	Val
		35					40						45		
Asp	Pro	Thr	Cys	Pro	Leu	Ser	Asn	Pro	Gly	Thr	Gln	Val	Tyr	Glu	
	50					55				60					
Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Glu	Asn	Asn	Asn	Asn
65					70				75					80	
Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln	Asp	Ser	Asn	Arg	Phe	Phe	Thr
			85					90						95	
Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	Lys	Ile

100					105					110						
Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Glu	Lys	Lys	
115					120					125						
Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp	Ala	Glu	Arg	Asp	His	Phe	Val	
130					135					140						
Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Ala	Glu	Asp	Glu	
145					150					155					160	
Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp	Arg	Gly	Pro	Val	Arg	Thr	Val	
165					170					175						
Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Lys	Leu	
180					185					190						
Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Thr	Met	Ala	Leu	
195					200					205						
Met	Asp	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Ser	Lys	Gln	
210					215					220						
Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Leu	
225					230					235					240	
Lys	Gly	Pro	Thr	Asp	Gly	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	His	
245					250					255						
Phe	Tyr	Thr	Val	Ile	Pro	His	Asn	Phe	Gly	His	Ser	Gln	Pro	Pro	Pro	
260					265					270						
Ile	Asn	Ser	Pro	Glu	Leu	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	
275					280					285						
Leu	Ala	Asp	Ile	Glu	Leu	Ala	Gln	Ala	Leu	Gln	Ala	Val	Ser	Glu	Gln	
290					295					300						
Glu	Lys	Thr	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	
305					310					315					320	
Leu	Leu	Lys	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly	Ala	Pro	Glu	Tyr	
325					330					335						
Lys	Val	Ile	Gln	Thr	Tyr	Leu	Glu	Gln	Thr	Gly	Ser	Asn	His	Arg	Cys	
340					345					350						
Pro	Thr	Leu	Gln	His	Ile	Trp	Lys	Val	Asn	Gln	Glu	Gly	Glu	Glu	Asp	
355					360					365						
Arg	Phe	Gln	Ala	His	Ser	Lys	Leu	Gly	Asn	Arg	Lys	Leu	Leu	Trp	His	
370					375					380						
Gly	Thr	Asn	Met	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	
385					390					395					400	
Ile	Met	Pro	His	Ser	Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	
405					410					415						
Ser	Glu	Asn	Ser	Lys	Ser	Ala	Gly	Tyr	Val	Ile	Gly	Met	Lys	Cys	Gly	

420	425	430
Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg		
435	440	445
Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro		
450	455	460
Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr		
465	470	475
Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln		
485	490	495
Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln		
500	505	510
Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu		
515	520	525
Leu Glu Val His Leu *		
530		

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 221..1843
- (D) OTHER INFORMATION: /product= "Poly ADP Ribose Polymerase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGGGACTGGT CGCCTGACTC GGCCTGCCCC AGCCTCTGCT TCACCCCACT GGTGGCCAAA	60
TAGCCGATGT CTAATCCCC ACACAAGCTC ATCCCCGGCC TCTGGGATTG TTGGGAATTC	120
TCTCCCTAAT TCACGCCTGA GGCTCATGGA GAGTTGCTAG ACCTGGGACT GCCCTGGGAG	180
GCGCACACAA CCAGGCCGGG TGGCAGCCAG GACCTCTCCC ATG TCC CTG CTT TTC	235
Met Ser Leu Leu Phe	
535	
TTG GCC ATG GCT CCA AAG CCG AAG CCC TGG GTA CAG ACT GAG GGC CCT	283

Leu	Ala	Met	Ala	Pro	Lys	Pro	Lys	Pro	Trp	Val	Gln	Thr	Glu	Gly	Pro		
540					545					550					555		
GAG	AAG	AAG	AAG	GGC	CGG	CAG	GCA	GGA	AGG	GAG	GAG	GAC	CCC	TTC	CGC		331
Glu	Lys	Lys	Lys	Gly	Arg	Gln	Ala	Gly	Arg	Glu	Glu	Asp	Pro	Phe	Arg		
				560					565					570			
TCC	ACC	GCT	GAG	GCC	CTC	AAG	GCC	ATA	CCC	GCA	GAG	AAG	CGC	ATA	ATC		379
Ser	Thr	Ala	Glu	Ala	Leu	Lys	Ala	Ile	Pro	Ala	Glu	Lys	Arg	Ile	Ile		
			575					580					585				
CGC	GTG	GAT	CCA	ACA	TGT	CCA	CTC	AGC	AGC	AAC	CCC	GGG	ACC	CAG	GTG		427
Arg	Val	Asp	Pro	Thr	Cys	Pro	Leu	Ser	Ser	Asn	Pro	Gly	Thr	Gln	Val		
		590					595					600					
TAT	GAG	GAC	TAC	AAC	TGC	ACC	CTG	AAC	CAG	ACC	AAC	ATC	GAG	AAC	AAC		475
Tyr	Glu	Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Glu	Asn	Asn		
	605					610					615						
AAC	AAC	AAG	TTC	TAC	ATC	ATC	CAG	CTG	CTC	CAA	GAC	AGC	AAC	CGC	TTC		523
Asn	Asn	Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln	Asp	Ser	Asn	Arg	Phe		
	620				625					630					635		
TTC	ACC	TGC	TGG	AAC	CGC	TGG	GGC	CGT	GTG	GGA	GAG	GTC	GGC	CAG	TCA		571
Phe	Thr	Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser		
				640					645					650			
AAG	ATC	AAC	CAC	TTC	ACA	AGG	CTA	GAA	GAT	GCA	AAG	AAG	GAC	TTT	GAG		619
Lys	Ile	Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Glu		
			655					660					665				
AAG	AAA	TTT	CGG	GAA	AAG	ACC	AAG	AAC	AAC	TGG	GCA	GAG	CGG	GAC	CAC		667
Lys	Lys	Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp	Ala	Glu	Arg	Asp	His		
		670					675					680					
TTT	GTG	TCT	CAC	CCG	GGC	AAG	TAC	ACA	CTT	ATC	GAA	GTA	CAG	GCA	GAG		715
Phe	Val	Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Ala	Glu		
	685					690					695						
GAT	GAG	GCC	CAG	GAA	GCT	GTG	GTG	AAG	GTG	GAC	AGA	GGC	CCA	GTG	AGG		763
Asp	Glu	Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp	Arg	Gly	Pro	Val	Arg		
	700				705					710					715		
ACT	GTG	ACT	AAG	CGG	GTG	CAG	CCC	TGC	TCC	CTG	GAC	CCA	GCC	ACG	CAG		811
Thr	Val	Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln		
				720					725					730			
AAG	CTC	ATC	ACT	AAC	ATC	TTC	AGC	AAG	GAG	ATG	TTC	AAG	AAC	ACC	ATG		859
Lys	Leu	Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Thr	Met		
			735					740					745				
GCC	CTC	ATG	GAC	CTG	GAT	GTG	AAG	AAG	ATG	CCC	CTG	GGA	AAG	CTG	AGC		907
Ala	Leu	Met	Asp	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Ser		
		750					755					760					
AAG	CAA	CAG	ATT	GCA	CGG	GGT	TTC	GAG	GCC	TTG	GAG	GCG	CTG	GAG	GAG		955
Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu		
	765					770					775						

GCC CTG AAA GGC CCC ACG GAT GGT GGC CAA AGC CTG GAG GAG CTG TCC	1003
Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser	
780 785 790 795	
TCA CAC TTT TAC ACC GTC ATC CCG CAC AAC TTC GGC CAC AGC CAG CCC	1051
Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro	
800 805 810	
CCG CCC ATC AAT TCC CCT GAG CTT CTG CAG GCC AAG AAG GAC ATG CTG	1099
Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu	
815 820 825	
CTG GTG CTG GCG GAC ATC GAG CTG GCC CAG GCC CTG CAG GCA GTC TCT	1147
Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser	
830 835 840	
GAG CAG GAG AAG ACG GTG GAG GAG GTG CCA CAC CCC CTG GAC CGA GAC	1195
Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp	
845 850 855	
TAC CAG CTT CTC AAG TGC CAG CTG CAG CTG CTA GAC TCT GGA GCA CCT	1243
Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro	
860 865 870 875	
GAG TAC AAG GTG ATA CAG ACC TAC TTA GAA CAG ACT GGC AGC AAC CAC	1291
Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His	
880 885 890	
AGG TGC CCT ACA CTT CAA CAC ATC TGG AAA GTA AAC CAA GAA GGG GAG	1339
Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu	
895 900 905	
GAA GAC AGA TTC CAG GCC CAC TCC AAA CTG GGT AAT CGG AAG CTG CTG	1387
Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu	
910 915 920	
TGG CAT GGC ACC AAC ATG GCC GTG GTG GCC GCC ATC CTC ACT AGT GGG	1435
Trp His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly	
925 930 935	
CTC CGC ATC ATG CCA CAT TCT GGT GGG CGT GTT GGC AAG GGC ATC TAC	1483
Leu Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr	
940 945 950 955	
TTT GCC TCA GAG AAC AGC AAG TCA GCT GGA TAT GTT ATT GGC ATG AAG	1531
Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys	
960 965 970	
TGT GGG GCC CAC CAT GTC GGC TAC ATG TTC CTG GGT GAG GTG GCC CTG	1579
Cys Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu	
975 980 985	
GGC AGA GAG CAC CAT ATC AAC ACG GAC AAC CCC AGC TTG AAG AGC CCA	1627
Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro	
990 995 1000	
CCT CCT GGC TTC GAC AGT GTC ATT GCC CGA GGC CAC ACC GAG CCT GAT	1675
Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp	

1005	1010	1015	
CCG ACC CAG GAC ACT GAG TTG GAG CTG GAT GGC CAG CAA GTG GTG GTG			1723
Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val			
1020	1025	1030	1035
CCC CAG GGC CAG CCT GTG CCC TGC CCA GAG TTC AGC AGC TCC ACA TTC			1771
Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe			
1040	1045		1050
TCC CAG AGC GAG TAC CTC ATC TAC CAG GAG AGC CAG TGT CGC CTG CGC			1819
Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg			
1055	1060		1065
TAC CTG CTG GAG GTC CAC CTC TGA GTGCCCCGCC TGTCCCCCGG GGTCTGCAA			1873
Tyr Leu Leu Glu Val His Leu *			
1070	1075		
GGCTGGACTG TGATCTTCAA TCATCCTGCC CATCTCTGGT ACCCCTATAT CACTCCTTTT			1933
TTTCAAGAAT ACAATACGTT GTTGTTAACT ATAGTCACCA TGCTGTACAA GATCCCTGAA			1993
CTTATGCCTC CTAAGTAAAA TTTTGTATTC TTTGACACAT CTGCCCAGTC CCTCTCCTCC			2053
CAGCCCATGG TAACCAGCAT TTGACTCTTT ACTTGATATAA GGGCAGCTTT TATAGGTTCC			2113
ACATGTAAGT GAGATCATGC AGTGTTTGTC TTTCTGTGCC TGGCTTATTT CACTCAGCAT			2173
AATGTGCACC GGGTTCACCC ATGTTTTTCAT AAATGACAAG ATTTCTCCTT TAAAAA			2233
AAAAA			2265

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Ser	Leu	Leu	Phe	Leu	Ala	Met	Ala	Pro	Lys	Pro	Lys	Pro	Trp	Val
1					5				10					15	
Gln	Thr	Glu	Gly	Pro	Glu	Lys	Lys	Lys	Gly	Arg	Gln	Ala	Gly	Arg	Glu
		20						25					30		
Glu	Asp	Pro	Phe	Arg	Ser	Thr	Ala	Glu	Ala	Leu	Lys	Ala	Ile	Pro	Ala
		35					40					45			
Glu	Lys	Arg	Ile	Ile	Arg	Val	Asp	Pro	Thr	Cys	Pro	Leu	Ser	Ser	Asn
	50					55					60				
Pro	Gly	Thr	Gln	Val	Tyr	Glu	Asp	Tyr	Asn	Cys	Thr	Leu	Asn	Gln	Thr
65					70					75				80	
Asn	Ile	Glu	Asn	Asn	Asn	Asn	Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln

85										90					95				
Asp	Ser	Asn	Arg	Phe	Phe	Thr	Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly				
			100					105					110						
Glu	Val	Gly	Gln	Ser	Lys	Ile	Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala				
		115					120					125							
Lys	Lys	Asp	Phe	Glu	Lys	Lys	Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp				
	130					135					140								
Ala	Glu	Arg	Asp	His	Phe	Val	Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile				
145					150					155					160				
Glu	Val	Gln	Ala	Glu	Asp	Glu	Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp				
				165					170					175					
Arg	Gly	Pro	Val	Arg	Thr	Val	Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu				
			180					185					190						
Asp	Pro	Ala	Thr	Gln	Lys	Leu	Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met				
		195					200						205						
Phe	Lys	Asn	Thr	Met	Ala	Leu	Met	Asp	Leu	Asp	Val	Lys	Lys	Met	Pro				
	210					215					220								
Leu	Gly	Lys	Leu	Ser	Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu				
225					230					235					240				
Glu	Ala	Leu	Glu	Glu	Ala	Leu	Lys	Gly	Pro	Thr	Asp	Gly	Gly	Gln	Ser				
				245					250					255					
Leu	Glu	Glu	Leu	Ser	Ser	His	Phe	Tyr	Thr	Val	Ile	Pro	His	Asn	Phe				
			260					265						270					
Gly	His	Ser	Gln	Pro	Pro	Pro	Ile	Asn	Ser	Pro	Glu	Leu	Leu	Gln	Ala				
		275					280						285						
Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	Ile	Glu	Leu	Ala	Gln	Ala				
	290					295					300								
Leu	Gln	Ala	Val	Ser	Glu	Gln	Glu	Lys	Thr	Val	Glu	Glu	Val	Pro	His				
305					310					315					320				
Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	Lys	Cys	Gln	Leu	Gln	Leu	Leu				
				325					330					335					
Asp	Ser	Gly	Ala	Pro	Glu	Tyr	Lys	Val	Ile	Gln	Thr	Tyr	Leu	Glu	Gln				
			340					345					350						
Thr	Gly	Ser	Asn	His	Arg	Cys	Pro	Thr	Leu	Gln	His	Ile	Trp	Lys	Val				
		355					360						365						
Asn	Gln	Glu	Gly	Glu	Glu	Asp	Arg	Phe	Gln	Ala	His	Ser	Lys	Leu	Gly				
	370					375						380							
Asn	Arg	Lys	Leu	Leu	Trp	His	Gly	Thr	Asn	Met	Ala	Val	Val	Ala	Ala				
385					390					395					400				
Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser	Gly	Gly	Arg	Val				

405	410	415
Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr		
420	425	430
Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu		
435	440	445
Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro		
450	455	460
Ser Leu Lys Ser Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly		
465	470	475
His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly		
485	490	495
Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe		
500	505	510
Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser		
515	520	525
Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu *		
530	535	540

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mus musculus

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 112..1710

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCCGGCTTTC ACTTTTCTG CTGCCTCGGG GAACACCTCG AGCCAACTGC TTCCTAACTC	60
AGGGTGGGCA GAACTGACGG GATCTAAGCT TCTGCATCTC TGAGGAGAAC C ATG GCT	117
Met Ala	
CCA AAA CGA AAG GCC TCT GTG CAG ACT GAG GGC TCC AAG AAG CAG CGA	165
Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg	
545 550 555	

CAA GGG ACA GAG GAG GAG GAC AGC TTC CGG TCC ACT GCC GAG GCT CTC	213
Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu	
560 565 570 575	
AGA GCA GCA CCT GCT GAT AAT CGG GTC ATC CGT GTG GAC CCC TCA TGT	261
Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys	
580 585 590	
CCA TTC AGC CGG AAC CCC GGG ATA CAG GTC CAC GAG GAC TAT GAC TGT	309
Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys	
595 600 605	
ACC CTG AAC CAG ACC AAC ATC GGC AAC AAC AAC AAC AAG TTC TAT ATT	357
Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile	
610 615 620	
ATC CAA CTG CTG GAG GAG GGT AGT CGC TTC TTC TGC TGG AAT CGC TGG	405
Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp	
625 630 635	
GGC CGC GTG GGA GAG GTG GGC CAG AGC AAG ATG AAC CAC TTC ACC TGC	453
Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys	
640 645 650 655	
CTG GAA GAT GCA AAG AAG GAC TTT AAG AAG AAA TTT TGG GAG AAG ACT	501
Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu Lys Thr	
660 665 670	
AAA AAC AAA TGG GAG GAG CGG GAC CGT TTT GTG GCC CAG CCC AAC AAG	549
Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys	
675 680 685	
TAC ACA CTT ATA GAA GTC CAG GGA GAA GCA GAG AGC CAA GAG GCT GTA	597
Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val	
690 695 700	
GTG AAG GCC TTA TCT CCC CAG GTG GAC AGC GGC CCT GTG AGG ACC GTG	645
Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val	
705 710 715	
GTC AAG CCC TGC TCC CTA GAC CCT GCC ACC CAG AAC CTT ATC ACC AAC	693
Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn	
720 725 730 735	
ATC TTC AGC AAA GAG ATG TTC AAG AAC GCA ATG ACC CTC ATG AAC CTG	741
Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu	
740 745 750	
GAT GTG AAG AAG ATG CCC TTG GGA AAG CTG ACC AAG CAG CAG ATT GCC	789
Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala	
755 760 765	
CGT GGC TTC GAG GCC TTG GAA GCT CTA GAG GAG GCC ATG AAA AAC CCC	837
Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro	
770 775 780	
ACA GGG GAT GGC CAG AGC CTG GAA GAG CTC TCC TCC TGC TTC TAC ACT	885
Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr	

785	790	795	
GTC ATC CCA CAC AAC TTC	GGC CGC AGC CGA CCC CCG CCC ATC AAC TCC		933
Val Ile Pro His Asn Phe	Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser		
800	805 810 815		
CCT GAT GTG CTT CAG GCC AAG AAG GAC ATG CTG CTG GTG CTA GCG GAC			981
Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp			
820	825 830		
ATC GAG TTG GCG CAG ACC TTG CAG GCA GCC CCT GGG GAG GAG GAG GAG			1029
Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu			
835	840 845		
AAA GTG GAA GAG GTG CCA CAC CCA CTG GAT CGA GAC TAC CAG CTC CTC			1077
Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu			
850	855 860		
AGG TGC CAG CTT CAA CTG CTG GAC TCC GGG GAG TCC GAG TAC AAG GCA			1125
Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala			
865	870 875		
ATA CAG ACC TAC CTG AAA CAG ACT GGC AAC AGC TAC AGG TGC CCA AAC			1173
Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn			
880	885 890 895		
CTG CGG CAT GTT TGG AAA GTG AAC CGA GAA GGG GAG GGA GAC AGG TTC			1221
Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe			
900	905 910		
CAG GCC CAC TCC AAA CTG GGC AAT CGG AGG CTG CTG TGG CAC GGC ACC			1269
Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr			
915	920 925		
AAT GTG GCC GTG GTG GCT GCC ATC CTC ACC AGT GGG CTC CGA ATC ATG			1317
Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met			
930	935 940		
CCA CAC TCG GGT GGT CGT GTT GGC AAG GGT ATT TAT TTT GCC TCT GAG			1365
Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu			
945	950 955		
AAC AGC AAG TCA GCT GGC TAT GTT ACC ACC ATG CAC TGT GGG GGC CAC			1413
Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His			
960	965 970 975		
CAG GTG GGC TAC ATG TTC CTG GGC GAG GTG GCC CTC GGC AAA GAG CAC			1461
Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His			
980	985 990		
CAC ATC ACC ATC GAT GAC CCC AGC TTG AAG AGT CCA CCC CCT GGC TTT			1509
His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe			
995	1000 1005		
GAC AGC GTC ATC GCC CGA GGC CAA ACC GAG CCG GAT CCC GCC CAG GAC			1557
Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp			
1010	1015 1020		
ATT GAA CTT GAA CTG GAT GGG CAG CCG GTG GTG GTG CCC CAA GGC CCG			1605

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Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro
1025                      1030                      1035

CCT GTG CAG TGC CCG TCA TTC AAA AGC TCC AGC TTC AGC CAG AGT GAA      1653
Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu
1040                      1045                      1050                      1055

TAC CTC ATA TAC AAG GAG AGC CAG TGT CGC CTG CGC TAC CTG CTG GAG      1701
Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu
                      1060                      1065                      1070

ATT CAC CTC TAAGCTGCTT GCCCTCCCTA GGTCCAAGCC      1740
Ile His Leu

```

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 533 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
 1              5              10              15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
          20              25              30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
          35              40              45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
          50              55              60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
          65              70              75              80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
          85              90              95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
          100              105              110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
          115              120              125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
          130              135              140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
          145              150              155              160

Ala Val Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg
          165              170              175

Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile

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			180					185					190				
Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Ala	Met	Thr	Leu	Met		
			195			200			205								
Asn	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln		
			210			215			220								
Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys		
			225			230			235			240					
Asn	Pro	Thr	Gly	Asp	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe		
			245			250			255								
Tyr	Thr	Val	Ile	Pro	His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile		
			260			265			270								
Asn	Ser	Pro	Asp	Val	Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu		
			275			280			285								
Ala	Asp	Ile	Glu	Leu	Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu		
			290			295			300								
Glu	Glu	Lys	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln		
			305			310			315			320					
Leu	Leu	Arg	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr		
			325			330			335								
Lys	Ala	Ile	Gln	Thr	Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys		
			340			345			350								
Pro	Asn	Leu	Arg	His	Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp		
			355			360			365								
Arg	Phe	Gln	Ala	His	Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His		
			370			375			380								
Gly	Thr	Asn	Val	Ala	Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg		
			385			390			395			400					
Ile	Met	Pro	His	Ser	Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala		
			405			410			415								
Ser	Glu	Asn	Ser	Lys	Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly		
			420			425			430								
Gly	His	Gln	Val	Gly	Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys		
			435			440			445								
Glu	His	His	Ile	Thr	Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro		
			450			455			460								
Gly	Phe	Asp	Ser	Val	Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala		
			465			470			475			480					
Gln	Asp	Ile	Glu	Leu	Glu	Leu	Asp	Gly	Gln	Pro	Val	Val	Val	Pro	Gln		
			485			490			495								
Gly	Pro	Pro	Val	Gln	Cys	Pro	Ser	Phe	Lys	Ser	Ser	Ser	Phe	Ser	Gln		

(2) INFORMATION FOR SEQ ID NO: 9:

(A) LENGTH: 1587 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mus musculus

(A) NAME/KEY: CDS

(B) LOCATION:1..1584

ATG Met	GCT Ala	CCA Pro	AAA Lys	CGA Arg	AAG Lys	GCC Ala	TCT Ser	GTG Val	CAG Gln	ACT Thr	GAG Glu	GGC Gly	TCC Ser	AAG Lys	AAG Lys	48
535			540			545										
CAG Gln 550	CGA Arg	CAA Gln	GGG Gly	ACA Thr	GAG Glu	GAG Glu	GAG Glu	GAC Asp	AGC Ser	TTC Phe	CGG Arg	TCC Ser	ACT Thr	GCC Ala	GAG Glu	96
555			560			565										
GCT Ala	CTC Leu	AGA Arg	GCA Ala	GCA Ala	CCT Pro	GCT Ala	GAT Asp	AAT Asn	CGG Arg	GTC Val	ATC Ile	CGT Arg	GTG Val	GAC Asp	CCC Pro	144
570			575			580										
TCA Ser	TGT Cys	CCA Pro	TTC Phe	AGC Ser	CGG Arg	AAC Asn	CCC Pro	GGG Gly	ATA Ile	CAG Gln	GTC Val	CAC His	GAG Glu	GAC Asp	TAT Tyr	192
585			590			595										
GAC Asp	TGT Cys	ACC Thr	CTG Leu	AAC Asn	CAG Gln	ACC Thr	AAC Asn	ATC Ile	GGC Gly	AAC Asn	AAC Asn	AAC Asn	AAC Asn	AAG Lys	TTC Phe	240
600			605			610										
TAT Tyr	ATT Ile	ATC Ile	CAA Gln	CTG Leu	CTG Leu	GAG Glu	GAG Glu	GGT Gly	AGT Ser	CGC Arg	TTC Phe	TTC Phe	TGC Cys	TGG Trp	AAT Asn	288
615			620			625										
CGC Arg 630	TGG Trp	GGC Gly	CGC Arg	GTG Val	GGA Gly	GAG Glu	GTG Val	GGC Gly	CAG Gln	AGC Ser	AAG Lys	ATG Met	AAC Asn	CAC His	TTC Phe	336
635			640			645										

ACC TGC CTG GAA GAT GCA AAG AAG GAC TTT AAG AAG AAA TTT TGG GAG	384
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu	
650 655 660	
AAG ACT AAA AAC AAA TGG GAG GAG CGG GAC CGT TTT GTG GCC CAG CCC	432
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro	
665 670 675	
AAC AAG TAC ACA CTT ATA GAA GTC CAG GGA GAA GCA GAG AGC CAA GAG	480
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu	
680 685 690	
GCT GTA GTG AAG GTG GAC AGC GGC CCT GTG AGG ACC GTG GTC AAG CCC	528
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro	
695 700 705	
TGC TCC CTA GAC CCT GCC ACC CAG AAC CTT ATC ACC AAC ATC TTC AGC	576
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser	
710 715 720 725	
AAA GAG ATG TTC AAG AAC GCA ATG ACC CTC ATG AAC CTG GAT GTG AAG	624
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys	
730 735 740	
AAG ATG CCC TTG GGA AAG CTG ACC AAG CAG CAG ATT GCC CGT GGC TTC	672
Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe	
745 750 755	
GAG GCC TTG GAA GCT CTA GAG GAG GCC ATG AAA AAC CCC ACA GGG GAT	720
Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp	
760 765 770	
GGC CAG AGC CTG GAA GAG CTC TCC TCC TGC TTC TAC ACT GTC ATC CCA	768
Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro	
775 780 785	
CAC AAC TTC GGC CGC AGC CGA CCC CCG CCC ATC AAC TCC CCT GAT GTG	816
His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val	
790 795 800 805	
CTT CAG GCC AAG AAG GAC ATG CTG CTG GTG CTA GCG GAC ATC GAG TTG	864
Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu	
810 815 820	
GCG CAG ACC TTG CAG GCA GCC CCT GGG GAG GAG GAG GAG AAA GTG GAA	912
Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu Lys Val Glu	
825 830 835	
GAG GTG CCA CAC CCA CTG GAT CGA GAC TAC CAG CTC CTC AGG TGC CAG	960
Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Arg Cys Gln	
840 845 850	
CTT CAA CTG CTG GAC TCC GGG GAG TCC GAG TAC AAG GCA ATA CAG ACC	1008
Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr	
855 860 865	
TAC CTG AAA CAG ACT GGC AAC AGC TAC AGG TGC CCA AAC CTG CGG CAT	1056
Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His	

870	875	880	885	
GTT TGG AAA GTG AAC CGA GAA GGG GAG GGA GAC AGG TTC CAG GCC CAC				1104
Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His	890	895	900	
TCC AAA CTG GGC AAT CGG AGG CTG CTG TGG CAC GGC ACC AAT GTG GCC				1152
Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala	905	910	915	
GTG GTG GCT GCC ATC CTC ACC AGT GGG CTC CGA ATC ATG CCA CAC TCG				1200
Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser	920	925	930	
GGT GGT CGT GTT GGC AAG GGT ATT TAT TTT GCC TCT GAG AAC AGC AAG				1248
Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys	935	940	945	
TCA GCT GGC TAT GTT ACC ACC ATG CAC TGT GGG GGC CAC CAG GTG GGC				1296
Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly	950	955	960	965
TAC ATG TTC CTG GGC GAG GTG GCC CTC GGC AAA GAG CAC CAC ATC ACC				1344
Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr	970	975	980	
ATC GAT GAC CCC AGC TTG AAG AGT CCA CCC CCT GGC TTT GAC AGC GTC				1392
Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val	985	990	995	
ATC GCC CGA GGC CAA ACC GAG CCG GAT CCC GCC CAG GAC ATT GAA CTT				1440
Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu	1000	1005	1010	
GAA CTG GAT GGG CAG CCG GTG GTG GTG CCC CAA GGC CCG CCT GTG CAG				1488
Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln	1015	1020	1025	
TGC CCG TCA TTC AAA AGC TCC AGC TTC AGC CAG AGT GAA TAC CTC ATA				1536
Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile	1030	1035	1040	1045
TAC AAG GAG AGC CAG TGT CGC CTG CGC TAC CTG CTG GAG ATT CAC CTC				1584
Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu	1050	1055	1060	
TAA				1587

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys

1	5	10	15
Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu	20	25	30
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro	35	40	45
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr	50	55	60
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe	65	70	75
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn	85	90	95
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe	100	105	110
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu	115	120	125
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro	130	135	140
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu	145	150	155
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro	165	170	175
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser	180	185	190
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys	195	200	205
Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe	210	215	220
Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp	225	230	235
Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro	245	250	255
His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val	260	265	270
Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu	275	280	285
Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu Lys Val Glu	290	295	300
Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln	305	310	315
Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr			

	325		330		335
Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His					
	340		345		350
Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His					
	355		360		365
Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala					
	370		375		380
Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser					
	385		390		395
Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys					
	405		410		415
Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His Gln Val Gly					
	420		425		430
Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr					
	435		440		445
Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val					
	450		455		460
Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu					
	465		470		475
Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln					
	485		490		495
Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile					
	500		505		510
Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu					
	515		520		525

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: YES
- (ix) FEATURE:
 - (A) NAME/KEY: Region
 - (B) LOCATION: 2
 - (D) OTHER INFORMATION: /note= "Xaa steht fuer 1 bis 5
andere Aminosaeuren"
- (ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:3
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:1
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:6
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder Val"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:9
- (D) OTHER INFORMATION:/note= "Xaa steht fuer 1 bis 5 andere Aminosaeuren"

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:10
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Ser oder Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Gly Xaa Xaa Xaa Gly Lys
 1 5 10 15
 Gly Ile Tyr Phe Ala
 20

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:

- 74 -

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

(A) NAME/KEY: Region

(B) LOCATION:1

(D) OTHER INFORMATION:/note= "Xaa steht fuer Leu oder
Val"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa
1				5				10					15	
Xaa Xaa Xaa Xaa Xaa Leu														
20														

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

(A) NAME/KEY: Region

(B) LOCATION:21

(D) OTHER INFORMATION:/note= "Xaa steht fuer Asp oder
Glu"

(ix) FEATURE:

(A) NAME/KEY: Region

(B) LOCATION:22

(D) OTHER INFORMATION:/note= "Xaa steht fuer 10 oder 11
andere Aminosaeuren"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Tyr	Xaa	Xaa
1				5				10					15		
Gln Leu Leu Xaa Xaa Xaa Trp Gly Arg Val Gly															
20 25															

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Ala	Xaa	Xaa	Xaa	Phe	Xaa	Lys	Xaa	Xaa	Xaa	Xaa	Lys	Thr	Xaa	Asn	Xaa
1				5				10						15	
Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Pro	Xaa	Lys			
				20				25							

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

(A) NAME/KEY: Region
(B) LOCATION: 4
(D) OTHER INFORMATION:/note= "Xaa steht fuer Ile oder
Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Gln	Xaa	Leu	Xaa	Xaa	Xaa	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5				10						15	
Met	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Leu	Gly	Lys	Leu
				20				25					30		
Xaa	Xaa	Xaa	Gln	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu
			35				40								

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Phe	Tyr	Thr	Xaa	Ile	Pro	His	Xaa	Phe	Gly	Xaa	Xaa	Xaa	Pro	Pro
1				5					10					15

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Lys	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Leu	Xaa	Asp	Ile	Glu	Xaa	Ala	Xaa	Xaa
1				5				10						15	

Leu

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Gly	Xaa	Xaa	Xaa	Leu	Xaa	Glu	Val	Ala	Leu	Gly
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:14
- (D) OTHER INFORMATION:/note= "Xaa steht fuer 7 bis 9
andere Aminosaeuren"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Gly Xaa Xaa Ser Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Leu Xaa
1 5 10 15

Gly Xaa Xaa Val
20

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: YES

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION:2
- (D) OTHER INFORMATION:/note= "Xaa steht fuer Tyr oder
Phe"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Glu Xaa Xaa Xaa Tyr Xaa Xaa Xaa Gln Xaa Xaa Xaa Xaa Tyr Leu Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
1 5 10 15

Leu Asn Glu Ser

20

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Lys	Thr	Glu	Leu	Gln	Ser	Pro	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg
1				5					10					15	
Asn	Leu	His	Cys												
			20												

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Cys	Lys	Gly	Arg	Gln	Ala	Gly	Arg	Glu	Glu	Asp	Pro	Phe	Arg	Ser	Thr
1				5					10					15	
Ala	Glu	Ala	Leu	Lys											
			20												

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu
1 5 10 15
Glu Ala Leu Lys
20

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15
Ala Leu Lys

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15
Ala Met Lys